WHAT IS CLAIMED IS:

1	1. A method for high information resolution of at least one analyte in				
2	a sample comprising the steps of:				
3	a) exposing the analyte to at least two different selectivity				
4	conditions, each selectivity condition defined by the combination of an adsorbent and an				
5	eluant, to allow retention of the analyte by the adsorbent; and				
6	b) detecting retained analyte under the different selectivity				
7	conditions by desorption spectrometry;				
8	whereby detection of retained analyte under the different selectivity				
9	conditions provides a high information resolution of the analyte.				
1	2. The method of claim 1 wherein each different selectivity condition				
2	is defined at a different predetermined, addressable location for parallel processing.				
1	3. The method of claim 1 comprising the steps of:				
2	i) exposing the analyte to a first selectivity condition at a				
3	defined location to allow retention of the analyte by the adsorbent;				
4	ii) detecting retained analyte under the first selectivity				
5	condition by desorption spectrometry;				
6	iii) washing the adsorbent under a second, different				
7	selectivity condition at the defined location to allow retention of the analyte to the				
8	adsorbent; and				
9	iv) detecting retained analyte under the second selectivity				
10	condition by desorption spectrometry.				
1	4. The method of claim 1 wherein the analyte is an organic				
2	biomolecule.				
1	5 The method of claim 1 wherein the analyte is a virus or a cell				

1	_	6.	The method of claim 1 wherein the adsorbent comprises an anion, a			
2	cation, a hyd	drophot	pic interaction adsorbent, a polypeptide, a nucleic acid, a			
3	carbohydrate	e, a lec	tin, a dye, a reducing agent, a hydrocarbon or a combination thereof.			
1		7.	The method of claim 1 wherein the different selectivity conditions			
2	comprise dif	ferent l	oinding conditions.			
	÷					
1		8.	The method of claim 1 wherein the different selectivity conditions			
2	comprise dif	comprise different elution conditions.				
1		9.	The method of claim 1 wherein the step of detecting comprises			
2	detecting the	mass	of the analyte by laser desorption mass spectrometry.			
1		10.	The method of claim 1 wherein selectivity conditions are selected to			
2	optimize reto	ention o	of analyte by an adsorbent.			
1	•	11.	The method of claim 1 wherein the adsorbent is attached to a			
2	substrate co	mprisin	g glass, ceramic, a magnetic material, an organic polymer, a			
3 .	conducting p	oolymei	, a native biopolymer, a metal, a metal coated with an organic			
4	polymer or	a comb	ination thereof.			
1	•	12.	The method of claim 1 wherein the adsorbent is in the form of a			
2	microemulsi	on, a la	itex, a layer or a bead.			
1		13.	The method of claim 2 wherein the locations are arranged in a line,			
2	an orthogon	al array	or a circle.			
1		14.	The method of claim 2 wherein the adsorbents are located on a			
2	substrate at different locations before the analytes are exposed to the selectivity					
3	conditions.					
1		15.	The method of claim 2 wherein the adsorbents are located on a			

substrate at different locations after the analytes are exposed to the selectivity conditions.

1		16.	The method of claim 2 wherein at least one analyte is more than			
2	one analyte.					
1		17.	The method of claim 2 wherein the plurality of selectivity			
2	conditions a	re defin	ed by at different adsorbents and the same eluant.			
1		18.	The method of claim 2 further comprising the step of providing a			
2	substrate comprising adsorbents at addressable locations, each adsorbent being an					
3	adsorbent from a selectivity condition identified to retain the analyte.					
•		•				
1	1	19.	The method of claim 2 comprising the steps of:			
2			a) exposing a sample comprising the analytes to a first selectivity			
3	condition to allow retention of analytes by a first adsorbent and to create un-retained					
4	sample;					
5			b) collecting the un-retained sample comprising analytes, exposing			
6	the un-retair	ned sam	ple to a second selectivity condition to allow retention of analytes by			
7	a second adsorbent and to create a second un-retained sample; and					
8			c) detecting retained analyte under the different selectivity			
9	conditions b	ption spectrometry.				
1		20.	The method of claim 4 wherein the organic biomolecule is an			
2	enzyme, an immunoglobulin, a cell surface receptor or an intracellular receptor.					
1		21.	The method of claim 8 wherein the elution conditions differ			
2	according to pH, buffering capacity, ionic strength, a water structure characteristic,					
3	detergent type, detergent strength, hydrophobicity or dielectric constant.					
1		22.	The method of claim 18 wherein the plurality of selectivity			
2	conditions a	re defin	ned by the same eluant.			
1		23.	The method of claim 19 further comprising the steps of collecting			

the second un-retained sample.

1	24. A substrate for desorption spectrometry comprising an adsorbent				
2	whose binding characteristics vary in a gradient along one or more linear axes.				
1	25. A method for preparative purification of an analyte from an impure				
2	sample comprising the steps of:				
3	a) exposing the sample to a substrate under a plurality of different				
4	selectivity conditions; detecting retained analyte under the different selectivity conditions				
5	by desorption spectrometry; and identifying selectivity conditions under which the analyte				
6	is retained;				
7	b) purifying the analyte by repeating, for a plurality of different				
8	identified selectivity conditions, a sequence of steps comprising:				
9	i) exposing the sample to an adsorbent under the identified				
10	selectivity condition to allow retention of the analyte by the adsorbent;				
11	ii) separating the analyte from an impurity that is not				
12	retained by the substrate; and				
13	iii) collecting the analyte from the adsorbent;				
14	whereby the analyte is purified.				
÷					
1	26. A method for selecting identity candidates for an analyte protein				
2	comprising the steps of:				
3	a) determining a value set specifying match parameters for at least				
4	a first and second physico-chemical characteristic of a protein analyte in a sample by i)				
5	exposing the analyte to a plurality of different selectivity conditions, wherein adsorption				
6	of the protein analyte to the substrate is mediated by a basis of attraction that identifies a				
7.	physico-chemical characteristic of the protein analyte; and ii) detecting retained analyte				
8	under the different selectivity conditions by desorption spectrometry; and				
9	b) performing, in a programmable digital computer, the steps of:				
10	i) accessing a database comprising, for each member of a				
11	set of reference polypeptides, a value set specifying at least a first and second physico-				
12	chemical characteristic of the reference polypeptides;				
13	ii) accessing the value set specifying the physico-chemical				
14	characteristics of the protein analyte;				

iii) sorting from the database, reference polypeptides having value sets within the match parameters;

whereby the sorted reference polypeptides provide identity candidates for the protein analyte and unsorted reference polypeptides provide non-identity candidates for the protein analyte.

- 27. The method of claim 26 wherein at least one physico-chemical characteristic is molecular mass.
- 28. The method of claim 26 wherein the database comprises, for each member of the set of reference polypeptides, an amino acid sequence of the polypeptide or a nucleotide sequence encoding the amino acid sequence of the polypeptide, and wherein the performing step further comprises providing code that derives the physicochemical characteristics of a reference polypeptide from the amino acid sequence of the polypeptide.

5

6

1

2

2

3

5

8

1 2

3

4

- 29. The method of claim 27 wherein at least one of the physico-chemical characteristics is hydrophobicity, pI, number of coordinate covalent bonding residues or charge.
- 30. A method of detecting an enzyme in a sample comprising the steps of:
- a) providing a solid phase comprising an adsorbent and an enzyme substrate bound to the adsorbent, wherein the activity of the enzyme on the enzyme substrate produces a product having a characteristic molecular mass;
 - b) exposing the substrate to the sample; and
 - c) detecting the product by desorption spectrometry; whereby detecting the product provides a detection of the enzyme.
- 31. The method of claim 30 for determining the amount of the enzyme wherein the step of detecting comprises detecting an amount of the product, and comparing the detected amount to a standard that relates the detected amount to an amount of the enzyme in the sample.